



SEQUENCE LISTING

<110> Labas, Yuliia Aleksandrovich
Gurskaya, Nadezda Georgievna
Yanushevich, Yuriy
Fradkov, Arcady Fedorovich
Lukyanov, Konstantin
Lukyanov, Sergey
Matz, Mikhail Vladimirovich

<120> NOVEL CHROMOPHORES/FLUOROPHORES AND
METHODS FOR USING THE SAME

<130> CLON-090

<140> 10/757, 356
<141> 2004-01-13

<150> 60/332, 980
<151> 2001-11-13

<150> PCT/US02/36499
<151> 2002-11-12

<160> 28

<170> FastSEQ for Windows Version 4.0

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<211> 868
<212> DNA
<213> Heteractis crispa

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aacgaccaca acttcaagtg cactgcagaa ggaaaaggag aaccatacaa aggctcacaa 180
agcctgacga tcaccgtAAC tgaaggaggt cctctgccat ttgccttcga cattcttca 240
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gatagtgtta gtgacgatga gaagaccatt gagcagcacc agaatgtgag ggcaagctac 720
ttcaatgata gtggaaaatg atcatttcct tattgatttc aatgttaggg cattcagttt 780
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ttgaagtcaa taaatagcta agcactac 868

<210> 2
<211> 225
<212> PRT
<213> Heteractis crispa

<400> 2

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 Gly Lys Val Asn Asp His Asn Phe Lys Cys Thr Ala Glu Gly Lys Gly
 20 25 30
 Glu Pro Tyr Lys Gly Ser Gln Ser Leu Thr Ile Thr Val Thr Glu Gly
 35 40 45
 Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Arg Tyr
 50 55 60
 Gly Asn Lys Val Phe Ala Lys Tyr Pro Lys Asp His Pro Asp Phe Phe
 65 70 75 80
 Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Val Ser Asn Tyr
 85 90 95
 Glu Asp Gly Gly Val Leu Thr Val Lys Gln Glu Thr Ser Leu Glu Gly
 100 105 110
 Asp Cys Ile Ile Cys Lys Ile Lys Ala His Gly Thr Asn Phe Pro Ala
 115 120 125
 Asp Gly Pro Val Met Gln Lys Arg Thr Asn Gly Trp Glu Pro Ser Thr
 130 135 140
 Glu Thr Val Ile Pro Arg Gly Gly Ile Leu Met Arg Asp Val Pro
 145 150 155 160
 Ala Leu Lys Leu Leu Gly Asn Lys Gly His Leu Leu Cys Val Met Glu
 165 170 175
 Thr Thr Tyr Lys Ser Lys Lys Gly Glu Pro Ala Lys Pro His Phe
 180 185 190
 His His Leu Arg Met Glu Lys Asp Ser Val Ser Asp Asp Glu Lys Thr
 195 200 205
 Ile Glu Gln His Glu Asn Val Arg Ala Ser Tyr Phe Asn Asp Ser Gly
 210 215 220
 Lys
 225

<210> 3
 <211> 845
 <212> DNA
 <213> Dendronephthya sp

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 attgaagggg aaggaaaaagg aaggccctac gaaggcacac agaccttgaa cctgacagtg 180
 aaagaaggcg cgccctctccc attttcttac gacatcttga caacacgattt gcaactacgga 240
 aacagagtat tcactgaata cccagcagat atcacggatt atttcaagca atcatttctt 300
 gaaggatatt cctgggaaag aaccatgact tatgaagaca agggcattt taccatcaga 360
 agcgacataa gcttggaaagg tgactgctt ttccaaaaca ttctttttaa tgggatgaac 420
 tttcccccaa atggtccagt tatgcagaag aaaactttga agtgggaacc atccacagag 480
 aagctgcacg tgcgtgatgg gttgcttgc ggtaatatta acatggctt gctgcttggaa 540
 ggaggtggac attacctgtg tgacttcaaa actacttaca aagcgaagaa ggttggtag 600
 ttgccagatt atcatttgt ggaccatcg attgagatct tgagtaatga cagcgattac 660
 aacaaagtga agctgtacga gcatggggtt gctcgctatt ctccgttgcc caagtcaggc 720
 ctggtagagg ttcaaggaa agccataatg actgcataaga taaacatgta gtgaagacca 780
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 ttgggg 845

<210> 4
 <211> 236
 <212> PRT
 <213> Dendronephthya sp

<400> 4

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Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Glu Gly Lys Gly Arg
20 25 30
Pro Tyr Glu Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala
35 40 45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ala Leu His Tyr Gly
50 55 60
Asn Arg Val Phe Thr Glu Tyr Pro Ala Asp Ile Thr Asp Tyr Phe Lys
65 70 75 80
Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Thr Tyr Glu
85 90 95
Asp Lys Gly Ile Cys Thr Ile Arg Ser Asp Ile Ser Leu Glu Gly Asp
100 105 110
Cys Phe Phe Gln Asn Ile Arg Phe Asn Gly Met Asn Phe Pro Pro Asn
115 120 125
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
130 135 140
Lys Leu His Val Arg Asp Gly Leu Leu Val Gly Asn Ile Asn Met Ala
145 150 155 160
Leu Leu Leu Glu Gly Gly His Tyr Leu Cys Asp Phe Lys Thr Thr
165 170 175
Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Phe Val Asp
180 185 190
His Arg Ile Glu Ile Leu Ser Asn Asp Ser Asp Tyr Asn Lys Val Lys
195 200 205
Leu Tyr Glu His Gly Val Ala Arg Tyr Ser Pro Leu Pro Lys Ser Gly
210 215 220
Leu Val Glu Val Gln Gly Lys Ala Ile Met Thr Ala
225 230 235

<210> 5

<211> 851

<212> DNA

<213> Zoaanthus sp

<400> 5

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tgcgtcgatg gacataagtt tgtaatcgag ggcaacggca atggaaatcc tttcaaaggg 180
aaacagttta ttaatctgtg tgtgattgaa ggaggaccac tgccattctc cgaagacata 240
ttgtctgctg cgtttgacta cgaaaacagg ctcttcactg aatatcctga aggcatagtt 300
gactatttca agaactcgtg tcctgctgaa tatacgtggc acaggtctt tcgctttgaa 360
gatggagcag tttgcatatg cagtgcagat ataacagtaa atgtaggaa aaactgcatt 420
tatcatgagt ccacgttttga tggagtgaac ttccctgctg atggacctgt gatgaaaaag 480
atgacaacta attgggaacc gtcctgcgag aaaatcatac caataaaatag tcagaagata 540
ttaaaagggg atgtctccat gtacccctt ctgaaggatg gtgggcgtta ccgctgccag 600
tttgacacaa ttacaaaggc aaagactgag caaaaagaaa tgccggactg gcacttcattc 660
cagcataaggc tcaaccgtga agaccgcagc gatgctaaga atcagaaatg gcaactgata 720
gaacatgcta ttgcattcccg atctgcttta ccctgataac aaaggagttg ctattgcattg 780
tgcattgcata ttacgctgat aaaaatgttag tttaacatg caattgtatg tgcattgcaca 840
ttaccctgtat a 851

<210> 6

<211> 231

<212> PRT
<213> Zoanthus sp

<400> 6
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Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Glu Gly Asn
20 25 30
Gly Asn Gly Asn Pro Phe Lys Gly Lys Gln Phe Ile Asn Leu Cys Val
35 40 45
Ile Glu Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Ala
50 55 60
Phe Asp Tyr Gly Asn Arg Leu Phe Thr Glu Tyr Pro Glu Gly Ile Val
65 70 75 80
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp His Arg Ser
85 90 95
Phe Arg Phe Glu Asp Gly Ala Val Cys Ile Cys Ser Ala Asp Ile Thr
100 105 110
Val Asn Val Arg Glu Asn Cys Ile Tyr His Glu Ser Thr Phe Tyr Gly
115 120 125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn
130 135 140
Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Ile Asn Ser Gln Lys Ile
145 150 155 160
Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg
165 170 175
Tyr Arg Cys Gln Phe Asp Thr Ile Tyr Lys Ala Lys Thr Glu Pro Lys
180 185 190
Glu Met Pro Asp Trp His Phe Ile Gln His Lys Leu Asn Arg Glu Asp
195 200 205
Arg Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Ile Glu His Ala Ile
210 215 220
Ala Ser Arg Ser Ala Leu Pro
225 230

<210> 7
<211> 1178
<212> DNA
<213> Scolymia cubensis

<400> 7
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ctacccaacat gcagcgtgct gggatgaagg ttaaggaaca tatgaagatc aaactgcgtt 180
tgggagggtac tgtaaacgga aagcatttcg cggtaatgg gacaggagac ggctaccctt 240
atcaggaaaa acagattttg aaacttatcg tcgaaggcag cgaacctctg ctttcgcctt 300
ttgatatctt gtcagcagca ttccagtatg gcaacaggc attcaccgaa tacccaacag 360
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gtttcacctt cgaagatggg gccatttgcg tcgcccaccaa cgatataacg atggttggtg 480
gtgagttca gtatgatatt cgatttgatg gtctgaactt ccctgaagat ggtccagtg 540
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tgctgaaggg tgaggttaac atggctctgt tgcttcaaga caaaagccat taccgttgcg 660
acctcaaaaac tacttacaaa gctaagaata atgtgccgca tcctccaggc taccactatg 720
tggatcactg cattgaaata ctcgaagaac gtaaggatca cguttaagctg cgggagcatg 780
ctaaagctcg ttctagcctg tcacccatca gtcggaaaaga acgaaaggct taggtgatag 840
tcaaaaagac aacaagacga aaatgaaagg tggcattgt tagaattga tatttcgat 900
tcaatgattc gttaaaggat ttgcttaggg ctagctaaca ggttaacatc ataaggatag 960

agattycgtt gcggagtttag aaccttwata tttccgaat tccamctaga gtcgttgaga 1020
aatttattag agactagctt tagagttact tttgtggaaa aaaaggttc catttttgc 1080
gttattacag cattaaagc ataggaatag agattcggtt atggaaaata acagtaggaa 1140
aatacgttgtt gaaaataaac ttgttgcga aaaaaaaaaa 1178

<210> 8
<211> 234
<212> PRT
<213> Scolymia cubensis

<400> 8
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Arg Met Gly Gly Thr Val Asn Gly Lys His Phe Ala Val Asn Gly Thr
20 25 30
Gly Asp Gly Tyr Pro Tyr Gln Gly Lys Gln Ile Leu Lys Leu Ile Val
35 40 45
Glu Gly Ser Glu Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Ala Ala
50 55 60
Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Thr Glu Ile Ala
65 70 75 80
Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Ser Trp Glu
85 90 95
Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr Asn Asp
100 105 110
Ile Thr Met Val Gly Gly Glu Phe Gln Tyr Asp Ile Arg Phe Asp Gly
115 120 125
Leu Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr Val Lys
130 135 140
Trp Glu Pro Ser Thr Glu Ile Met Tyr Met Gln Asn Gly Val Leu Lys
145 150 155 160
Gly Glu Val Asn Met Ala Leu Leu Leu Gln Asp Lys Ser His Tyr Arg
165 170 175
Cys Asp Leu Lys Thr Thr Tyr Lys Ala Lys Asn Asn Val Pro His Pro
180 185 190
Pro Gly Tyr His Tyr Val Asp His Cys Ile Glu Ile Leu Glu Glu Arg
195 200 205
Lys Asp His Val Lys Leu Arg Glu His Ala Lys Ala Arg Ser Ser Leu
210 215 220
Ser Pro Thr Ser Ala Lys Glu Arg Lys Ala
225 230

<210> 9
<211> 819
<212> DNA
<213> Scolymia cubensis

<400> 9
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gatcacactg cgtatggacg gtgctgtaaa cgggaagccc ttgcgcgtta atggAACAGG 180
agatggcaac ccttatgggtg gaatacagag ttgaaagctt accgtcgatg gcaacaaacc 240
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cgaataaccca aaagagatat cagactattt caagcagtgc ttgagtttgcgagggggtt 360
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aaagatggtt ggcgtatgat ttcaatataa cattcgattt gatgggtgtga atttccctga 480
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ccattaccga tgtgacttca aaactactta caaagctaag aatcctgtcc cgccgacggc 660
gcttcagac taccactatg tggatcactg tattgaaatc accgaggaaa atagggatta 720
cgtaaagctg caggagtagt ctaaagctcg ttctggcctg cacctgccc aactgcaaaa 780
gtaaaggctt aggcatgt caagacgaca acgagaaga 819

<210> 10

<211> 235

<212> PRT

<213> Scolymia cubensis

<400> 10

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20 25 30
Gly Thr Gly Asp Gly Asn Pro Tyr Gly Gly Ile Gln Ser Leu Lys Leu
35 40 45
Thr Val Asp Gly Asn Lys Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser
50 55 60
Ala Ala Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Lys Glu
65 70 75 80
Ile Ser Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Thr
85 90 95
Trp Glu Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr
100 105 110
Asn Asp Ile Lys Met Val Gly Asp Glu Phe Gln Tyr Asn Ile Arg Phe
115 120 125
Asp Gly Val Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr
130 135 140
Val Lys Trp Glu Pro Ser Thr Glu Ile Met Arg Val Gln Gly Val
145 150 155 160
Leu Lys Gly Glu Val Asn Met Ala Leu Leu Leu Lys Asp Lys Ser His
165 170 175
Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Asn Pro Val Pro
180 185 190
Pro Thr Ala Leu Pro Asp Tyr His Tyr Val Asp His Cys Ile Glu Ile
195 200 205
Thr Glu Glu Asn Arg Asp Tyr Val Lys Leu Gln Glu Tyr Ala Lys Ala
210 215 220
Arg Ser Gly Leu His Leu Pro Glu Leu Gln Lys
225 230 235

<210> 11

<211> 807

<212> DNA

<213> Ricordea florida

<400> 11

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aaatcaagct tacattggtg ggcgttgta acgggcaccc attcaagatc attggggacg 120
gaaaaggcaa accctatgag ggatcgcagg attaacccct tgccgtggtg gaaggagggc 180
ctctgcctt ctcttatgat atcctgacaa cgatagttca ctatggcaac agggcatttg 240
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gatattcctg gcaaaggacc atgagtttg aagacggagg cgtttgcact gctacgagcc 360
atatcagggt ggatggcgcac acttcaatt atgacattca cttcatggga gcggatttcc 420
ctcttaatgg tccagtgtatc cagaaaagaa cagtgaaatg ggagccatcc actgagataa 480

tgtttcaatg tgatggattg ctgaggggtg atgttgcatt gtctctgttg ctgaaaggag 540
gcggccatta ccgatgtgac tttaaaacta ttataaacc caagaagaat gtcaagatgc 600
caggttacca ttttgtggac cactgcattt agataacgag tcaacaggac gattacaacg 660
tggttgagct gtacgagggt gctgtagccc actactctcc tctgcagaaa ccatgccaag 720
caaaggcata aagccaaaca acccaagagg acaacaagac atttaatcaa atcacatctt 780
tgtatttttg gtttagagttt aaaaaaa 807

<210> 12
<211> 231
<212> PRT
<213> Ricordea florida

<400> 12
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20 25 30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Ala Val Val Glu Gly Gly
35 40 45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ile Val His Tyr Gly
50 55 60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65 70 75 80
Gln Thr Cys Ser Gly Pro Gly Ala Gly Tyr Ser Trp Gln Arg Thr Met
85 90 95
Ser Phe Glu Asp Gly Gly Val Cys Thr Ala Thr Ser His Ile Arg Val
100 105 110
Asp Gly Asp Thr Phe Asn Tyr Asp Ile His Phe Met Gly Ala Asp Phe
115 120 125
Pro Leu Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
130 135 140
Ser Thr Glu Ile Met Phe Gln Cys Asp Gly Leu Leu Arg Gly Asp Val
145 150 155 160
Ala Met Ser Leu Leu Lys Gly Gly His Tyr Arg Cys Asp Phe
165 170 175
Lys Thr Ile Tyr Lys Pro Lys Lys Asn Val Lys Met Pro Gly Tyr His
180 185 190
Phe Val Asp His Cys Ile Glu Ile Thr Ser Gln Gln Asp Asp Tyr Asn
195 200 205
Val Val Glu Leu Tyr Glu Gly Ala Val Ala His Tyr Ser Pro Leu Gln
210 215 220
Lys Pro Cys Gln Ala Lys Ala
225 230

<210> 13
<211> 796
<212> DNA
<213> Ricordea florida

<400> 13
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taaaatggtg ggcgttgtta acgggcagtc atttcagatc gatggggaaag gaaaaggcaa 180
accttacgag ggatcacaga aattaaccct tgaagtgggt gaaggaggc ctctgctctt 240
ctcttatgat atcctgacaa cgatattca gtatggcaac agggcattcg tgaactaccc 300
aaaggacata ccagatattt tcaagcagac ctgctctggt cctgatggtg gatttccctg 360
gcaaaggacc atgacttatg aagacggagg ggtttgcact gtttcaaacc acatcagcgt 420

ggacggcgac acttttatt atgtgataag attaatgga gagaatttc ctccaaatgg 480
tccagtaatg cagaaaagaa cagtgaard ggagccatcc actgagataa tgtttgaacg 540
tgatggattg ctgaggggtg acattgccat gtctctgttgc ctgaaaggag gcggccatta 600
ccgatgtgac tttaaaacta tttatacacc caagaggaag gtcaacatgc caggttacca 660
ttttgtggac cactgcattt agatacagaa gcacgacaag gattacaaca tggctgtgct 720
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<210> 14
<211> 231
<212> PRT
<213> Ricordea florida

<400> 14

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Pro	Tyr	Glu	Gly	Ser	Gln	Lys	Leu	Thr	Leu	Glu	Val	Val	Glu	Gly	Gly
					35				40				45		
Pro	Leu	Leu	Phe	Ser	Tyr	Asp	Ile	Leu	Thr	Thr	Ile	Phe	Gln	Tyr	Gly
					50				55			60			
Asn	Arg	Ala	Phe	Val	Asn	Tyr	Pro	Lys	Asp	Ile	Pro	Asp	Ile	Phe	Lys
					65			70			75			80	
Gln	Thr	Cys	Ser	Gly	Pro	Asp	Gly	Gly	Phe	Ser	Trp	Gln	Arg	Thr	Met
					85				90				95		
Thr	Tyr	Glu	Asp	Gly	Gly	Val	Cys	Thr	Ala	Ser	Asn	His	Ile	Ser	Val
					100				105				110		
Asp	Gly	Asp	Thr	Phe	Tyr	Tyr	Val	Ile	Arg	Phe	Asn	Gly	Glu	Asn	Phe
					115				120				125		
Pro	Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Arg	Thr	Val	Lys	Trp	Glu	Pro
					130			135			140				
Ser	Thr	Glu	Ile	Met	Phe	Glu	Arg	Asp	Gly	Leu	Leu	Arg	Gly	Asp	Ile
					145			150			155			160	
Ala	Met	Ser	Leu	Leu	Lys	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp	Phe	
					165				170				175		
Lys	Thr	Ile	Tyr	Thr	Pro	Lys	Arg	Lys	Val	Asn	Met	Pro	Gly	Tyr	His
					180			185				190			
Phe	Val	Asp	His	Cys	Ile	Glu	Ile	Gln	Lys	His	Asp	Lys	Asp	Tyr	Asn
					195				200			205			
Met	Ala	Val	Leu	Ser	Glu	Asp	Ala	Val	Ala	His	Asn	Ser	Pro	Leu	Glu
					210			215			220				
Lys	Lys	Ser	Gln	Ala	Lys	Ala									
					225			230							

<210> 15
<211> 795
<212> DNA
<213> Montastraea cavernosa

<400> 15

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caagctgcgt	at	ggaaggca	gtgtaaacgg	gcacaacttc	gt	atttgttgc	gagaaggaga	180
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gcctttcgcc	tac	gatatac	tgacaacagt	attccattac	gg	caataggg	tattcgcaaa	300
atacccaaaa	cat	atcccag	actattcaa	gcagatgtt	cct	gaggagt	attcctggaa	360

acgaaggcatg aatttcgaag gcggggcat ttgcaccgcc aggaacgaga taacaatgga 420
aggcgactgt ttttcaata aagttcgatt tgatggtgtg aactcccc ccaatggtcc 480
agtcatgcag aagaagacgc taaaaatggg gccatccact gaaaaaatgt atgtgcgtga 540
tggagtgtc acgggtgata tcaacatggc tttgttgctt gaaggaggtg gccattaccg 600
atgtgacttc agaactactt acagagctaa gaagaagggt gtcaagttac cagattatca 660
ctttgaggat cactccattg agatttgcg ccatgacaaa gaatacactg aggttaagct 720
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aaagccaaga ccaca 795

<210> 16

<211> 235

<212> PRT

<213> Montastraea cavernosa

<400> 16

Arg Leu Ile Ser Tyr Phe Thr Ser Thr Ile Met Ser Val Ile Lys Ser
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20 25 30
Phe Val Ile Val Gly Glu Gly Lys Pro Tyr Glu Gly Thr Gln
35 40 45
Ser Met Asp Leu Thr Val Lys Glu Gly Ala Pro Leu Pro Phe Ala Tyr
50 55 60
Asp Ile Met Thr Thr Val Phe His Tyr Gly Asn Arg Val Phe Ala Lys
65 70 75 80
Tyr Pro Lys His Ile Pro Asp Tyr Phe Lys Gln Met Phe Pro Glu Glu
85 90 95
Tyr Ser Trp Glu Arg Ser Met Asn Phe Glu Gly Gly Ile Cys Thr
100 105 110
Ala Arg Asn Glu Ile Thr Met Glu Gly Asp Cys Phe Phe Asn Lys Val
115 120 125
Arg Phe Asp Gly Val Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
130 135 140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp
145 150 155 160
Gly Val Leu Thr Gly Asp Ile Asn Met Ala Leu Leu Leu Glu Gly Gly
165 170 175
Gly His Tyr Arg Cys Asp Phe Arg Thr Thr Tyr Arg Ala Lys Lys Lys
180 185 190
Gly Val Lys Leu Pro Asp Tyr His Phe Glu Asp His Ser Ile Glu Ile
195 200 205
Leu Arg His Asp Lys Glu Tyr Thr Glu Val Lys Leu Tyr Glu His Ala
210 215 220
Glu Ala His Ser Gly Leu Pro Arg Val Ala Lys
225 230 235

<210> 17

<211> 1066

<212> DNA

<213> Montastraea cavernosa

<400> 17

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acatgaagat gaagctgcgt atgaaagggt ctgtaaacgg gcacaagttc gtgggtgaag 180
gagatgaaa aggaaaggct ttgcacggaa cacagactat ggaccttaca gtcataagaag 240
gcccaccatt gccttcgct tacgatatct tgacaacagt attcgattac ggcaacaggg 300

tattcgccaa atacccagaa gacatagcag attatttcaa gcagacgtt cctgagggg 360
acttctggaa acgaagcatg acatacgaag accaggcat ttgcacatgcc acaaacgaca 420
taacaatgtat ggaaggcgctc gacgactgtt ttgcctataa aattcgattt gatggtgtga 480
actttccctgc caatggtcca gttatgcaga ggaagacgct gaaatggag ccatccactg 540
agataatgtat tgccgtgtat ggagtgtca agggtgatgt taacatggct ctgttgctt 600
aaggagggtgg ccattaccga tgtgacttca aaactactta caaagctaag aaggttgtcc 660
ggttgcaga ctatcactt gtggaccatc gcattgagat tgtgagccac gacaaagatt 720
acaacaaggta taagctgcac gagcatgccg aagctcgatca tggactgtca aggaaggcca 780
agtaaaggct taatgaaaag tcaagacgac aacgaggaga aacaaagtac tttttgtta 840
aatttgaagg catttactcg gaatttagtat ttgatactt cgattcaagg atttgttccg 900
ggatttggta gagactagct ctagagttgtt attttgtgaa aaaagatagt ttccagttt 960
tgccgggatta cagcatgggg atagacttt taaactcagt tgtggtcaaa tgcaagtaag 1020
aaaactgttag tgagaataaaa cttgttatcg aagccgaaaa aaaaaaa 1066

<210> 18

<211> 234

<212> PRT

<213> *Montastraea cavernosa*

<400> 18

Met	Thr	Ser	Val	Ala	Gln	Glu	Lys	Gly	Val	Ile	Lys	Pro	Asp	Met	Lys
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Met	Lys	Leu	Arg	Met	Glu	Gly	Ala	Val	Asn	Gly	His	Lys	Phe	Val	Val
					20				25					30	
Glu	Gly	Asp	Gly	Lys	Gly	Lys	Pro	Phe	Asp	Gly	Thr	Gln	Thr	Met	Asp
					35				40				45		
Leu	Thr	Val	Ile	Glu	Gly	Ala	Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu
					50				55				60		
Thr	Thr	Val	Phe	Asp	Tyr	Gly	Asn	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Glu
					65				70			75		80	
Asp	Ile	Ala	Asp	Tyr	Phe	Lys	Gln	Thr	Phe	Pro	Glu	Gly	Tyr	Phe	Trp
					85				90				95		
Glu	Arg	Ser	Met	Thr	Tyr	Glu	Asp	Gln	Gly	Ile	Cys	Ile	Ala	Thr	Asn
					100				105				110		
Asp	Ile	Thr	Met	Met	Glu	Gly	Val	Asp	Asp	Cys	Phe	Ala	Tyr	Lys	Ile
					115				120				125		
Arg	Phe	Asp	Gly	Val	Asn	Phe	Pro	Ala	Asn	Gly	Pro	Val	Met	Gln	Arg
					130				135				140		
Lys	Thr	Leu	Lys	Trp	Glu	Pro	Ser	Thr	Glu	Ile	Met	Tyr	Ala	Arg	Asp
					145				150			155		160	
Gly	Val	Leu	Lys	Gly	Asp	Val	Asn	Met	Ala	Leu	Leu	Leu	Glu	Gly	Gly
					165				170				175		
Gly	His	Tyr	Arg	Cys	Asp	Phe	Lys	Thr	Thr	Tyr	Lys	Ala	Lys	Lys	Val
					180				185				190		
Val	Arg	Leu	Pro	Asp	Tyr	His	Phe	Val	Asp	His	Arg	Ile	Glu	Ile	Val
					195				200				205		
Ser	His	Asp	Lys	Asp	Tyr	Asn	Lys	Val	Lys	Leu	His	Glu	His	Ala	Glu
					210				215				220		
Ala	Arg	His	Gly	Leu	Ser	Arg	Lys	Ala	Lys						
					225				230						

<210> 19

<211> 898

<212> DNA

<213> *Condylactis gigantea*

<400> 19

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 atccttgat caaggaaacc atgcgcagta aggtttacat ggaaggagat gttacaacc 120
 acgcctcaa gtgcactgca gtaggagaag gaaaaccata caaaggctca caagaccta 180
 cgattaccgt cactgaagga ggtcctctgc catttgcctt cgacattctt tcacacgcct 240
 ttcagtatgg caacaagggtg ttcaccgatt accccgacga tattcctgat ttcttaagc 300
 agtctctc ggtgggttt acttggagaa gagtaagcac statgacgt ggaggagttc 360
 tcacagttac ccaagacact agtctgaagg gagattgcat tatttgcac attaaagtcc 420
 atggactaa ctccccgaa aatggccgg tgatgcaaaa caagaccat ggatgggagc 480
 catccagcac taaaacgggtt attccacaag atggaggaat tggtgctgct cgatcacccg 540
 cactaaggct gcgtgataaa ggtcatctt tctgccacat ggaaacaact tacaagccaa 600
 acaaagaggt gaagctgcca gaactccact ttcatcattt gcgaatggaa aagctgagtg 660
 ttagtgacga tggaagagacc attaagcagc acgagtatgt ggtggctagc tactccaaag 720
 tgccttcgaa gataggacgt caatgatcat ttcccttatt aaatatcaat gatgtggctt 780
 tcaattttcc aaaattttgt taagacatag gtctttgga tttttgtaa ccccaacctt 840
 aattccaat aatttttgtt ggaaagtcaa ataaaaccag cttccctgg gccttaa 898

<210> 20

<211> 229

<212> PRT

<213> Condylactis gigantea

<400> 20

Met	Tyr	Pro	Trp	Ile	Lys	Glu	Thr	Met	Arg	Ser	Lys	Val	Tyr	Met	Glu
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Gly	Asp	Val	Asn	Asn	His	Ala	Phe	Lys	Cys	Thr	Ala	Val	Gly	Glu	Gly
															20
Lys	Pro	Tyr	Lys	Gly	Ser	Gln	Asp	Leu	Thr	Ile	Thr	Val	Thr	Glu	Gly
															35
Gly	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ser	His	Ala	Phe	Gln	Tyr
															50
Gly	Asn	Lys	Val	Phe	Thr	Asp	Tyr	Pro	Asp	Asp	Ile	Pro	Asp	Phe	Phe
															65
Lys	Gln	Ser	Leu	Ser	Asp	Gly	Phe	Thr	Trp	Arg	Arg	Val	Ser	Thr	Tyr
															85
Asp	Asp	Gly	Val	Leu	Thr	Val	Thr	Gln	Asp	Thr	Ser	Leu	Lys	Gly	
															100
Asp	Cys	Ile	Ile	Cys	Asn	Ile	Lys	Val	His	Gly	Thr	Asn	Phe	Pro	Glu
															115
Asn	Gly	Pro	Val	Met	Gln	Asn	Lys	Thr	Asp	Gly	Trp	Glu	Pro	Ser	Ser
															130
Thr	Glu	Thr	Val	Ile	Pro	Gln	Asp	Gly	Gly	Ile	Val	Ala	Ala	Arg	Ser
															145
Pro	Ala	Leu	Arg	Leu	Arg	Asp	Lys	Gly	His	Leu	Ile	Cys	His	Met	Glu
															165
Thr	Thr	Tyr	Lys	Pro	Asn	Lys	Glu	Val	Lys	Leu	Pro	Glu	Leu	His	Phe
															180
His	His	Leu	Arg	Met	Glu	Lys	Leu	Ser	Val	Ser	Asp	Asp	Gly	Lys	Thr
															195
Ile	Lys	Gln	His	Glu	Tyr	Val	Val	Ala	Ser	Tyr	Ser	Lys	Val	Pro	Ser
															210
Lys	Ile	Gly	Arg	Gln											
															225

<210> 21

<211> 1030

<212> DNA

<213> Agaricia fragilis

<400> 21

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tttctactct aaagaacgtc atcatcatcg ttatttatata ctccctgcgc acttgtgctg 120
tttggtcgaa ttcaaactct gaatccctt tcactaatgg gattgcagag gaaatgaaga 180
ctagggtaca tttggagggt actgttaacg ggcaactcct tacaattaaa ggcgaaggaa 240
gaggctaccc ttacaaagga gaacagtta tgagccttga ggtcgtaat ggtgctcc 300
tgccgttctc ttttgatatc ttgacaccag catttatgtt tggcaacaga gtgttacca 360
agtaccacc aaacatacca gactattca agcagacgtt tcctgaaggg tatcactggg 420
aaagaaacat tcccttgaa gatcaggccg cgtgcacggt aaccagccac ataagattgg 480
aagaggaaga gaggcggtt gtaaataacg ttagatttca ctgtgtgaac tttcccccta 540
atggtccagt catgcagagg aggatactga aatgggagcc atccactgag aacatttac 600
cgcgtgatgg gtttctggag ggccatgtt atatgactct tcgggttga ggaggtggct 660
attaccgagc ttagttcaaa agtacttaca aagggaagac cccagtcgc gacatgccag 720
acttcactt catagaccac cgcattgaga ttacggagca tgacgaagac tacaccaatg 780
ttgagctgca tgacgtatcc tgggctcggt actctatgtt gcccactatg taagcggaaa 840
aggcaaggca acaagacgca aaaccgcctt gtttgcctt tttcataaga gatttgacaa 900
ccgtggcttct ttgccattta atttgaatta gtttaaatta aatctttggg attgatgtag 960
acgcttggt tgctaagtaa gaaaacattt gtgatttatta aatttgcctt ctgaagcaaa 1020
aaaaaaaaaaaa 1030

<210> 22

<211> 259

<212> PRT

<213> Agaricia fragilis

<400> 22

Met	Ala	Ile	Ser	Thr	Leu	Lys	Asn	Val	Ile	Ile	Ile	Val	Ile	Ile	Tyr
1									10						15
Ser	Cys	Ser	Thr	Cys	Ala	Val	Trp	Ser	Asn	Ser	Asn	Ser	Glu	Ser	Ser
									25						30
Phe	Thr	Asn	Gly	Ile	Ala	Glu	Glu	Met	Lys	Thr	Arg	Val	His	Leu	Glu
									35						40
Gly	Thr	Val	Asn	Gly	His	Ser	Phe	Thr	Ile	Lys	Gly	Glu	Gly	Arg	Gly
									50						55
Tyr	Pro	Tyr	Lys	Gly	Glu	Gln	Phe	Met	Ser	Leu	Glu	Val	Val	Asn	Gly
									65						70
Ala	Pro	Leu	Pro	Phe	Ser	Phe	Asp	Ile	Leu	Thr	Pro	Ala	Phe	Met	Tyr
									85						90
Gly	Asn	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Pro	Asn	Ile	Pro	Asp	Tyr	Phe
									100						105
Lys	Gln	Thr	Phe	Pro	Glu	Gly	Tyr	His	Trp	Glu	Arg	Asn	Ile	Pro	Phe
									115						120
Glu	Asp	Gln	Ala	Ala	Cys	Thr	Val	Thr	Ser	His	Ile	Arg	Leu	Glu	Glu
									130						135
Glu	Glu	Arg	Arg	Phe	Val	Asn	Asn	Val	Arg	Phe	His	Cys	Val	Asn	Phe
									145						150
Pro	Pro	Asn	Gly	Pro	Val	Met	Gln	Arg	Arg	Ile	Leu	Lys	Trp	Glu	Pro
									165						170
Ser	Thr	Glu	Asn	Ile	Tyr	Pro	Arg	Asp	Gly	Phe	Leu	Glu	Gly	His	Val
									180						185
Asp	Met	Thr	Leu	Arg	Val	Glu	Gly	Gly	Tyr	Tyr	Arg	Ala	Glu	Phe	
									195						200
Lys	Ser	Thr	Tyr	Lys	Gly	Lys	Thr	Pro	Val	Arg	Asp	Met	Pro	Asp	Phe
									210						215
His	Phe	Ile	Asp	His	Arg	Ile	Glu	Ile	Thr	Glu	His	Asp	Glu	Asp	Tyr
									225						230
Thr	Asn	Val	Glu	Leu	His	Asp	Val	Ser	Trp	Ala	Arg	Tyr	Ser	Met	Leu
															235

Pro Thr Met

245

250

255

<210> 23
<211> 1024
<212> DNA
<213> Ricordea florida

<400> 23
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aaaattttac ttacttctt ccagcatgaa tgcacttcaa gaggaaatga aaatcaagct 120
tacaatggtg ggcgttgtt acggcagtc attaagatc gatgggaaag gaaaaggaa 180
accttacgag ggatcacagg aattgaccct taaagtggtg gaaggcgcc ctctgcttt 240
ctcttatgtat atcctgacaa cgatattca gtatggcaac agggattcg tgaactaccc 300
aaaggacata ccagatattt tcaagcaaac gtgttctggt cttgatggcg gatattcg 360
gcaaaggacc atgacttatg aggacggagg gtttgtact gctacaagca acgtcagcgt 420
ggtcggcgac acitccaatt atgaaattca ctttatgggg gcgaattttc ctccaaatgg 480
tccrgrtgatg cagaaaagaa cagtgaagtg ggagccctcc actgagataa tgtttgaacg 540
tgatggattt ctgaggggtg atgttccat gtctctgtt ctgaaaggag ggcaccatta 600
ccgatgtgac tttaaaacta ttataaaacc caacaagaag gtcaagctgc caggttacca 660
tttggac cactgcattt agataaagag tcaagagaat gattacaaca tggttgcgt 720
cttgaggat gctgttagcac actactctcc tctggagaaa aagagccagg caaaggcgta 780
aatccaaaca acctaagaag acgacaaggc attcaatcta atcgcatgtt tgaattttt 840
gttaggaatg tggtgggtca gacttaggtct agaacgttcc attttggctg gatttggttt 900
actcaggat agacaagaaaa aaaatctta atgacttggg ttggatttag cttcggcac 960
tgtcaattcc ggattcctta gaaatattt agaccaagcc ttttttgag ctgagaacgt 1020
aattc 1024

<210> 24
<211> 231
<212> PRT
<213> Ricordea florida

<400> 24
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Val Val Asn Gly Gln Ser Phe Lys Ile Asp Gly Lys Gly Lys Gly Lys
20 25 30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Lys Val Val Glu Gly Gly
35 40 45
Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
50 55 60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65 70 75 80
Gln Thr Cys Ser Gly Leu Asp Gly Gly Tyr Ser Trp Gln Arg Thr Met
85 90 95
Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Thr Ser Asn Val Ser Val
100 105 110
Val Gly Asp Thr Phe Asn Tyr Glu Ile His Phe Met Gly Ala Asn Phe
115 120 125
Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
130 135 140
Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Val
145 150 155 160
Pro Met Ser Leu Leu Leu Lys Gly Gly Asp His Tyr Arg Cys Asp Phe
165 170 175

Lys	Thr	Ile	Tyr	Lys	Pro	Asn	Lys	Lys	Val	Lys	Leu	Pro	Gly	Tyr	His
				180				185						190	
Phe	Val	Asp	His	Cys	Ile	Glu	Ile	Lys	Ser	Gln	Glu	Asn	Asp	Tyr	Asn
				195				200					205		
Met	Val	Ala	Leu	Phe	Glu	Asp	Ala	Val	Ala	His	Tyr	Ser	Pro	Leu	Glu
				210				215				220			
Lys	Lys	Ser	Gln	Ala	Lys	Ala									
				225				230							

<210> 25
<211> 913
<212> DNA
<213> Montastraea cavernosa

<400> 25
agagctgttag ggtgatatact tacttacgtc taccatcatg accagtgttg cacaggaaaa 60
gggtgtgatt aaaccagaca tgaagatgaa gctgcgtatg gaagggtctg taaacgggca 120
caagttcgta attgaaggag atggaaaagg gaagccttc gacggAACAC agactatgga 180
ccttacagtc atagaaggcg caccattgcc ttgcgttac gctatcttgc caacagtatt 240
cgattacggc aacagggtat tcgccaaata cccagaagac atagcagatt atttcaagca 300
gacatTTCT gaggggtact tctggaaacg aagcatgaca tacgaagagc agggcattt 360
catcgccaca aacgacataa caatgtgaa aggctgtcgac gactgtttt tctataaaat 420
tcgatttgat ggtgtgaaact ttccctgccaa tggtccagtt atgcagagga agacgctgaa 480
atgggagcca tccactgaga aaatgtatgc gcgtgtatggc gtgctgaaagg gtgatgttaa 540
catggctctg ttgttgcggag gaggtggcca ttaccgtatg gacttcaaaa ctacttacag 600
agctaagaag gttgtccagtt tgccagacta tcattttgtt gaccatcgca ttgagattgt 660
gagccacgac aaagattaca acaagggttaa gctgttatgag catggccaaag ctcatctgg 720
gctgccgagg caggccaaagt aaaggcttaa tggaaaagcca agacgacaac aaggagaaac 780
aaagtatttt ttttgttaaa tttcaaggca ttactcggtt attagtattt gatactttcg 840
attcaaggat ttgtttcggtt acttgtttaga gaccagctct agagttgtat tttgtgaaaa 900
aaagatagtt tcc 913

<210> 26
<211> 234
<212> PRT
<213> Montastraea cavernosa

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<400> 26
Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
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Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Ile
   20          25          30
Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
   35          40          45
Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Ala Ile Leu
   50          55          60
Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
   65          70          75          80
Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
   85          90          95
Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
  100          105         110
Asp Ile Thr Met Met Lys Gly Val Asp Asp Cys Phe Val Tyr Lys Ile
  115          120         125
Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
  130          135         140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Ala Arg Asp

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145	150	155	160
Gly Val Leu Lys Gly Asp Val Asn Met Ala		Leu Leu Leu Glu Gly Gly	
165	170	175	
Gly His Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Arg Ala Lys Lys Val			
180	185	190	
Val Gln Leu Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Val			
195	200	205	
Ser His Asp Lys Asp Tyr Asn Lys Val Lys Leu Tyr Glu His Ala Glu			
210	215	220	
Ala His Ser Gly Leu Pro Arg Gln Ala Lys			
225	230		

<210> 27
<211> 1133
<212> DNA
<213> Montastraea annularis

<400> 27

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atccaggtt	aaagcagcat	cctcagtgc	gaggctcat	tcacccttgtt	gatttggaaag	120
agagcagatc	gagaacacca	agagctgtat	tacgctaaaa	tcttacttgc	ctctaccacc	180
atgagtatga	ttaaaccaga	aatgaagatc	aagatgcgtt	tggacgggtgc	tgtaaacggg	240
cacaagttcg	tgattacagg	ggaaggaagc	ggcgagcctt	tcgaggggaaa	acagactatg	300
aacctgacag	tcatalogacgg	cgacccctgt	ccttcgtt	tcgacatctt	gacaacagca	360
ttcgattacg	gcacmagggt	attcgccaaa	taccagaag	acatcccaga	ctatttcaag	420
cagtcgttcc	ctgaggggtt	ttcttggaa	cgaagcatga	cttacgaaga	cgggggcatt	480
tgcatcgcca	caaatgacat	aaaaatggaa	ggcgactgct	tttcctatga	aattcgattt	540
gatgggtgt	acttcctgc	caatagtcca	gttatgcaga	agaagaccgt	gaaatgggag	600
ccatgcactg	rggaaatgtt	tgtgcgtat	ggagtgccta	aagggtgtct	taacatggct	660
ctgttgcctt	aaggagggtgg	ccatcccga	tgtgacttgc	aaactactta	caaagctaag	720
aagggtgtcc	agatgccaga	ctatcacttt	gtgaatcacc	gacttgagat	aacatggcat	780
gacgaggatt	acaacaatgt	taagctgtct	gagcatgcag	aagctcattt	tggactgcct	840
aggcaggcca	aataaaggct	tgacgaaaag	ccaaaacggc	aaagagtaca	agaaagtata	900
tataaatgtt	tatTTTCAA	ctgaaaaggca	ttccactcgg	aatttagtatt	tgataactttc	960
aattcaagga	tttattttgg	gatttgctag	ccactagctt	tattgttaaa	ttaagttaaa	1020
gacggtttag	catttttcg	gtattacaac	ataggcacag	acgtcttaac	cccagttagtg	1080
gtcaggtaca	agtaagaaaa	cttggtgag	aatagacttg	tagtcgaaaa	aaa	1133

<210> 28
<211> 224
<212> PRT
<213> Montastraea annularis

<220>
<221> VARIANT
<222> 65, 144
<223> Xaa = Any Amino Acid

<400> 28

Met Ser Met Ile Lys Pro Glu Met Lys Ile Lys Met Arg Met Asp Gly						
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Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Ser Gly Glu						
20	25	30				
Pro Phe Glu Gly Lys Gln Thr Met Asn Leu Thr Val Ile Asp Gly Gly						
35	40	45				
Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Ala Phe Asp Tyr Gly						
50	55	60				

Xaa Arg Val Phe Ala Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Phe Lys
65 70 75 80
Gln Ser Phe Pro Glu Gly Phe Ser Trp Glu Arg Ser Met Thr Tyr Glu
85 90 95
Asp Gly Gly Ile Cys Ile Ala Thr Asn Asp Ile Lys Met Glu Gly Asp
100 105 110
Cys Phe Ser Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe Pro Ala Asn
115 120 125
Ser Pro Val Met Gln Lys Lys Thr Val Lys Trp Glu Pro Cys Thr Xaa
130 135 140
Glu Met Tyr Val Arg Asp Gly Val Leu Lys Gly Gly Leu Asn Met Ala
145 150 155 160
Leu Leu Leu Glu Gly Gly His Phe Arg Cys Asp Leu Lys Thr Thr
165 170 175
Tyr Lys Ala Lys Lys Val Val Gln Met Pro Asp Tyr His Phe Val Asn
180 185 190
His Arg Leu Glu Ile Thr Trp His Asp Glu Asp Tyr Asn Asn Val Lys
195 200 205
Leu Ser Glu His Ala Glu Ala His Ser Gly Leu Pro Arg Gln Ala Lys
210 215 220